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GENOME ANNOUNCEMENT

Genome Sequence of *Bartonella birtlesii*, a Bacterium Isolated from Small Rodents of the Genus *Apodemus*

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***Bartonella birtlesii* is a facultative intracellular bacterium isolated from the blood of small mammals of the genus *Apodemus*. The present study reports the draft genome of *Bartonella birtlesii* strain IBS 135^T (CIP 106691^T).**

Bacteria of the genus *Bartonella* are facultative intracellular bacteria that use arthropod transmission and invasion of red blood cells as a parasitism strategy (8). *Bartonella* species belong to the α-2 subgroup of *Proteobacteria* and are fastidious Gram-negative bacteria highly adapted to their mammalian reservoir hosts, where they live within erythrocytes. To date, more than 30 *Bartonella* species have been isolated from mammals (including humans and domestic and wild animals), and half of them are considered emerging pathogens (6). *Bartonella birtlesii* has been isolated for the first time from the blood of small mammals of the genus *Apodemus* in France and the United Kingdom (1). Although its pathogenicity in humans is unknown, this bacterium has been mainly used as a model to study long-term bacteremia and erythrocyte adhesion and invasion in mice (2, 9). Using signature-tagged mutagenesis of this bacterium, components of the type IV secretion system (T4SS) Trw were identified as the molecular determinant for host-specific erythrocyte infection (9). Therefore, in order to be able to identify any disrupted genes in this signature-tagged mutagenesis library, we sequenced the genome of *B. birtlesii*.

Genomic DNA from *B. birtlesii* (strain IBS 325^T, CIP 106294^T) was fully sequenced by pyrosequencing using a Titanium genome sequencer (454 Life Sciences, Branford, CT) (5). A library of paired-end fragments was created following the manufacturer's instructions (454 Life Sciences). This library was sequenced using a GS Titanium sequencer (454 Life Sciences) (5).

Reads originated from the strain were assembled into contigs, and a scaffold was created using Newbler 2.53 (454 Life Sciences, Branford, CT). The assembly was verified using CLC Genomics software (CLC Bio, MA). Open reading frame (ORF) prediction was performed on the wild-type strain using PRODIGAL (3). Predicted proteins were compared against the GenBank nonredundant database using BLASTP (http://www.ncbi.nlm.nih.gov) for functional annotation. tRNAs and rRNAs were predicted using ARAGORN (4) and RNAMMER (3), respectively.

B. birtlesii draft genome sequencing generated one scaffold containing 35 contigs with an average coverage of 27-fold. The genome exhibits a total size of 1,833,875 bp and a G+C content of 37%. A total of 1,648 protein-coding ORFs with an average size of 871 bp were identified and cover 78.6% of the genome. Among those genes we found 106 ORFans (6.4% of the total gene content), 42 tRNAs, and two ribosomal operons with the 3 expected RNA genes (5S, 23S, and 16S). Other notable functional features were two type IV secretion system operons (VirB and Trw). We identified 1,250 orthologous genes between *B. birtlesii* and *Bartonella tribocorum*, the most closely related *Bartonella* species whose genome has been sequenced (7), using a reciprocal best BLAST hit strategy.

Nucleotide sequence accession numbers. The results from this whole-genome shotgun project have been deposited with DDBJ/EMBL/GenBank under the accession number AKIP00000000. The version described in this paper is the first version, AKIP01000000.

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